

C. Claims

The following is a complete listing of the claims, and replaces all earlier versions and listings.

1. (Currently Amended) An information processing method for designing a DNA probe, said method comprising:

a first counting step for counting, with regard to a first base sequence data group containing a target base sequence, the number of times of manifestation of each of a plurality of partial base sequences obtained from data of said target base sequence, and holding frequency information obtained by said counting;

a second counting step for counting, with regard to a second base sequence data group to be distinguished from said first base sequence data group, the number of times of manifestation of each of said plurality of partial base sequences, and holding frequency information obtained by said counting; and

~~a formation~~ an identification step for forming probe candidates based on frequency information held in said first and second counting steps.

2. (Currently Amended) An information processing method for designing a DNA probe according to claim 1, wherein said ~~formation~~ identification step for forming probe candidates based on frequency information held in said first and second counting steps comprises:

a display step for displaying frequency information held in said first and second counting steps, so as to be comparable with reference to said plurality of partial base sequences; and

a ~~formation~~ determining step for determining at least one of said plurality of partial base sequences according to instruction operations made by a user, and forming probe candidates based on the determined partial base sequences.

3. (Original) An information processing method for designing a DNA probe according to claim 2, further comprising in addition to said first and second counting steps, a third counting step for counting, with regard to said first base sequence data group and said second base sequence data group, the position and length of partial base sequences common to both, and holding information obtained thereby.

4. (Original) An information processing method for designing a DNA probe according to claim 3, wherein probe creating is performed with regard to regions between common base sequences obtained in said third counting step.

5. (Original) An information processing method for designing a DNA probe according to claim 3, wherein probe creating is performed with regard to all regions between common base sequences obtained in said third counting step.

6. (Currently Amended) An information processing method for designing a DNA probe according to claim 1, wherein said ~~formation~~ identification step for forming probe candidates based on frequency information held in said first and second counting steps comprises:

a searching step for searching for partial base sequences, which are used to identify probe candidates without having to search entire base sequences, wherein the frequency obtained in said first counting step exceeds a first predetermined value, and wherein the frequency obtained in said second counting step is smaller than a second predetermined value; and

~~a formation~~ an identifying step for forming probe candidates based on the partial base sequences searched in said searching step.

7. (Currently Amended) An information processing method for designing a DNA probe according to claim 6, further comprising a third counting step for counting[[,]] the position and length of partial base sequences common to said first base sequence group and said second base sequence group[[,]] and holding information obtained thereby; ~~wherein said searching step is a searching step for searching for partial base sequences wherein the frequency obtained in said first counting step exceeds a first predetermined value, and wherein the frequency obtained in said second counting step is smaller than [[a]] the second predetermined value, with regard to regions between common regions obtained in said third counting step.~~

8. (Currently Amended) An information processing method for designing a DNA probe according to claim 1, wherein said plurality of partial base sequences are obtained by acquiring a base sequence by extracting a predetermined number of bases from said target base sequence data, while shifting ~~the head~~ a start position ~~thereof~~ of a base sequence.

9. (Original) An information processing method for designing a DNA probe according to claim 1, wherein said first base sequence data group is base sequence data including a plurality of polymorphs of a target organism species, and wherein said second base sequence data group is base sequence data including a plurality of polymorphs of a organism species other than said target organism species.

10. (Currently Amended) An information processing method for designing a DNA probe according to claim 1, further comprising a first selecting step for selecting probe candidates to be used for a probe set with regard to probe candidates formed in said ~~forming~~ identification step, by adding and deleting bases at the head and end such that the melting temperature is around the same as that of other probes making up the probe set.

11. (Currently Amended) An information processing method for designing a DNA probe according to claim 1, further comprising a first selecting step for

calculating the probe melting temperature for the probe candidates formed in said ~~forming~~ identification step, and selecting probe candidates to be used for a probe set based on the calculated melting temperature.

12. (Currently Amended) An information processing method for designing a DNA probe according to claim 1, further comprising a second selecting step for calculating the probability of formation of secondary structures with regard to the probe candidates formed in said ~~forming~~ identification step, and selecting probe candidates to be used for a probe set based on the calculation results.

13. (Currently Amended) An information processing method for designing a DNA probe according to claim 1, further comprising a third selecting step for calculating a degree of matching with regard to the probe candidates formed in said ~~forming~~ identification step, and selecting probe candidates to be used for a probe set based on the degree of matching.

14. (Currently Amended) A DNA probe design device comprising:
first counting means for counting, with regard to a first base sequence data group containing a target base sequence, the number of times of manifestation of each of a plurality of partial base sequences obtained from data of said target base sequence, and holding frequency information obtained by said counting;

second counting means for counting, with regard to a second base sequence data group to be distinguished from said first base sequence data group, the number of times of manifestation of each of said plurality of partial base sequences, and holding frequency information obtained by said counting;

display means for displaying frequency information held by said first and second counting means, so as to be comparable with reference to said plurality of partial base sequences; and

~~formation~~ identification means for determining at least one of said plurality of partial base sequences according to instruction operations made by a user, and forming probe candidates based on the determined partial base sequences.

15. (Original) A DNA probe design device according to claim 14, further comprising in addition to said first and second counting means, third counting means for counting, with regard to said first base sequence data group and said second base sequence data group, the position and length of partial base sequences common to both, and holding information obtained thereby.

16. (Original) A DNA probe design device according to claim 15, wherein said display means add common information held by said third counting means to the frequency information held by said first and second counting means, and display the information so as to be comparable with reference to said plurality of partial base sequences.

17. (Original) A DNA probe design device according to claim 15, wherein probe creating is performed with regard to regions between common base sequences obtained in said third counting means.

18. (Currently Amended) A DNA probe design device comprising:
first counting means for counting, with regard to a first base sequence data group containing a target base sequence, the number of times of manifestation of each of a plurality of partial base sequences obtained from data of said target base sequence, and holding frequency information obtained by said counting;

second counting means for counting, with regard to a second base sequence data group to be distinguished from said first base sequence data group, the number of times of manifestation of each of said plurality of partial base sequences, and holding frequency information obtained by said counting;

searching means for searching for partial base sequences, which are used to identify probe candidates without having to search entire base sequences, wherein the frequency obtained by said first counting means exceeds a first predetermined value, and wherein the frequency obtained by said second counting means is smaller than a second predetermined value; and

~~formation~~ identification means for forming probe candidates based on the partial base sequences searched by said searching means.

19. (Currently Amended) A DNA probe design device comprising:

first counting means for counting, with regard to a first base sequence data group containing a target base sequence, the number of times of manifestation of each of a plurality of partial base sequences obtained from data of said target base sequence, and holding frequency information obtained by said counting;

second counting means for counting, with regard to a second base sequence data group to be distinguished from said first base sequence data group, the number of times of manifestation of each of said plurality of partial base sequences, and holding frequency information obtained by said counting;

third counting means for counting, with regard to said first base sequence data group and said second base sequence data group, the position and length of partial base sequences common to both, and holding information obtained thereby;

searching means for searching for, with regard to regions between common base sequences obtained by said third counting means, partial base sequences, which are used to identify probe candidates without having to search entire base sequences, wherein the frequency obtained by said first counting means exceeds a first predetermined value, and wherein the frequency obtained by said second counting means is smaller than a second predetermined value; and

~~formation~~ identification means for forming probe candidates based on the partial base sequences searched by said searching means.

20. (Currently Amended) A control program stored on a computer readable medium for causing a computer to execute the information processing method for designing a DNA probe according to claim 1.

21. (Original) A storage medium storing a control program for causing a computer to execute the information processing method for designing a DNA probe according to claim 1.

22. (Withdrawn) A DNA microarray having nucleic acid probes designed by the probe design method according to claim 1.

23. (Withdrawn) A nucleic acid testing method using the DNA microarray according to claim 22.